EDITORIAL

NUCLEIC ACIDS RESEARCH ANNUAL WEB SERVER ISSUE IN 2012

The 2012 Web Server Issue of *Nucleic Acids Research* is the 10th in a series of annual special issues dedicated to web-based software resources for analysis and visualization of molecular biology data. It is freely available online under NAR's open access policy. The present issue reports on 102 web servers.

Topics

This year's special emphasis is on analysis of next-generation sequencing data, including RNAseq analysis, genetic variation detectors and metagenomics; network and pathway analysis; and biological text mining. A total of 21 papers deal with these topics. The major categories of papers cover analysis involving DNA and RNA (13 papers); protein structure, docking and functional site prediction (38 papers); and gene set enrichment, gene function annotation and protein function annotation (11 papers).

The 2012 Web Server issue continues the presentation of two special categories, one for standalone programs that analyze high-throughput data, such as next-generation sequencing data and one for large collections of popular web services for automated analyses that can be utilized programmatically rather than through manual interaction with a web browser. Five papers fall in these categories.

Also included is the Bioinformatics Links Directory 2012 update by Michelle Brazas, Francis Ouellette and their colleagues at the Ontario Institute for Cancer Research. The directory, at http://bioinformatics.ca/links_directory, is a searchable compilation of web servers published in this and previous Web Server issues together with other useful tools, databases and resources for life sciences research.

Instructions for Submissions

To streamline the review process, authors are required to send a one-page summary of their web server to the editor, Dr Gary Benson (narwbsrv@bu.edu), for pre-approval prior to manuscript submission. For the 2012 issue, 289 summaries were submitted and 141 (49%) were approved for manuscript submission. Of those approved 102 (72%) were ultimately accepted for publication.

Review of a summary includes evaluation of the proposal and extensive testing of web server functionality. The key criteria for pre-approval are high scientific quality, wide interest, the ability to do computations on user-submitted data, and a well designed, well implemented and fully functional website. Note that there is a minimum 2-year interval before publication in the Web Server issue for web servers, or essentially similar web servers, that have been the subject of a previous publication, including publication in journals other than NAR.

With respect to the website, the following are guidelines for approval.

(i) It should have an easy-to-find submission page with a simple mechanism for loading test data and setting test parameters. The preferred method is one-click loading. Additional mechanisms that assist the user in submitting data should be implemented where appropriate. For example, automatic download of a pdb structure file once the user has entered the appropriate identifier.

(ii) Output should be dynamic and rich in detail. Wherever possible, supporting evidence used in calculations and/or links to external databases containing additional information should be provided. Numerical, textual and visual output should be mixed and any visualization tools that add information or increase the user's understanding should be utilized (for example the java plug-in tools jmol for structure visualization and jalview for sequence alignment visualization). Note that output which consists merely of a few numerical values, a static spreadsheet or a series of files to be opened in other programs will not be approved.

(iii) Web servers that do not finish their calculations immediately must implement a mechanism for returning results to the user. Notification by email may be provided as an option, but an alternative that returns a web link at the time of data submission, which the user can then bookmark and access at a later time, is required. This link should ideally report the status of the job (queued, running, finished). Websites that use a guest login will not be approved. Note that uploaded data and the results of analysis for each user must be private and not viewable by other users.

(iv) The website should be supported by an extensive help section or tutorial that guides the user through the submission process, contains details about input file formats and parameters, and importantly, explains the

meaning of the output. Whenever possible, the help pages should link to dynamic output examples similar to those provided by the website.

(v) Any proposal for a web server that is *predictive* must include details on validation of predictions from new data not used in training. N-fold cross validation methods will not be considered sufficient. Details should include the size and composition of the validation data set (number of positive and negative cases), and several measures of predictive performance, including sensitivity, specificity and precision. Proposals are regularly rejected for lack of adequate prediction validation information.

(vi) Websites not clearly designed to accept and analyze user-submitted data will be rejected. This applies to those established primarily for lookup or exploration in a data set, or serve the function of 'data aggregators'. Authors of websites that provide novel data should consider the NAR Database Issue as a possible venue (see the instructions at http://www.oxfordjournals.org/our_journals/nar/for_authors/msprep_database.html).

(vii) Proposals that describe a new analysis method are generally not appropriate for the Web Server issue because limited space makes adequate method description and validation problematic. Authors of such methods might instead consider sending their manuscript to NAR as a regular computational biology paper (see the instructions for authors at http://www.oxfordjournals.org/our_journals/nar/for_authors/criteria_scope.html#Computational%20Biology).

Special Emphasis for 2013

For the 2013 issue the topics of special emphasis will be analysis of next-generation sequencing data, network and pathway analysis; and biological text mining.

Deadlines for 2013

Authors wishing to submit manuscripts for the 2013 Web Server issue must submit their one page proposal along with the URL address of the fully functional website to narwbsrv@bu.edu by 31 December 2012. Detailed instructions and requirements are presented at http://www.oxfordjournals.org/nar/for_authors/submission_webserver.html. This information should be consulted before sending in the summary. The deadline for submission of articles is 31 January 2013.

Requirement for References Links

Manuscripts submitted for the 2013 issue must format their References section to include active links to electronic versions of the cited papers, including links to PubMed, PubMed Central and a DOI link. Instructions for incorporating these links into the manuscript are presented at http://www.oxfordjournals.org/nar/for_authors/submission_webserver.html.

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Executive Editor
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